

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: February 16, 2005, 16:12:05 ; Search time 69.2267 Seconds
(without alignments)
2810.909 Million cell updates/sec
Title: US-10-003-356-5
Perfect score: 1986
Sequence: 1 LPHSVCTDVCPPTGRGFVQ.....TVSTVLDDRVLVYMCPLKQLQ 380
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1906	96.0	755	2	Q8NGV9
2	1749	88.1	365	2	Q8TDU1
3	1450	73.0	428	2	Q70413
4	1444	72.7	912	2	Q70410
5	904.5	45.5	230	2	Q70414
6	791.5	39.9	458	2	Q93555
7	787.5	39.7	848	2	Q93553
8	775.5	39.0	362	2	Q9PSY1
9	775.5	39.0	408	2	Q93558
10	769.5	38.7	844	2	Q93552
11	755.5	38.0	350	2	Q93556
12	753.5	37.9	880	2	Q73639
13	751	37.8	875	2	Q73640
14	747	37.6	856	2	Q73638
15	736.5	37.1	1027	2	Q8J104
16	722	36.4	864	2	Q73637
17	715.5	36.0	783	2	Q8CDP3
18	714.5	36.0	1079	1	CASR MOUSE
19	714.5	36.0	1079	1	CASR RAT
20	713.5	35.9	1079	2	Q802A8
21	711.5	35.8	1078	1	CASR HUMAN
22	709.5	35.7	1085	1	CASR_BOVIN
23	702.5	35.4	868	2	Q73636
24	696.5	35.1	854	2	Q6UNX3
25	696	35.0	941	2	Q6XAF1
26	696	35.0	941	2	Q6XAF3
27	678.5	34.2	940	2	Q73635
28	675	34.0	940	2	Q90WL6
29	660	33.2	850	2	Q6XAF2
30	644	32.4	157	2	Q99PC0
31	640.5	32.3	866	2	Q35268

32	639.5	32.2	855	2	Q70409
33	638.5	32.2	855	2	Q6TAC4
34	636.5	32.0	845	2	Q80208
35	621.5	31.3	695	2	Q35272
36	620.5	31.2	339	2	Q70411
37	614.5	30.9	501	2	Q86UN7
38	612.5	30.8	852	2	Q35192
39	607.5	30.6	865	2	Q80209
40	606.5	30.5	667	2	Q35267
41	605.5	30.5	723	2	Q35193
42	605.5	30.5	779	2	Q35269
43	603.5	30.4	803	2	Q35191
44	600.5	30.2	768	2	Q35266
45	598.5	30.1	850	2	Q35189

ALIGNMENTS

RESULT 1

Q8NGV9	PRELIMINARY;	PRT;	755 AA.
ID	Q8NGV9		
AC	Q8NGV9;		
DT	01-OCT-2002 (Tremblrel. 22, Created)		
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)		
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)		
DE	Seven transmembrane helix receptor.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,		
RA	Tsutsui S., Aburatani H., Asai K., Akiyama Y.,		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB065664; BAC05890.1; -		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.		
DR	GO; GO:004872; F:receptor activity; IEA.		
DR	InterPro; IPR001828; ANF receptor.		
DR	InterPro; IPR000337; GPCR_Mgr.		
DR	Pfam; PF00003; 7tm 3; 1.		
DR	Pfam; PF01094; ANF receptor; 1.		
DR	PRINTS; PR00248; GPCRMR.		
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.		
KW	Receptor; Transmembrane.		
SQ	SEQUENCE 755 AA; 83791 MW; 04D56AD8917BD1F CRC64;		

Query Match 96.0%; Score 1906; DB 2; Length 755;
Best Local Similarity 99.7%; Pred. No. 1.5e-130;
Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	13	GTGRTGVQREPCICFADGHVSRKPGERECQCGEDYNSNAQSECVKEVYLAY	72
Db	388	GLRGFGVQREPCICFADGHVSRKPGERECQCGEDYNSNAQSECVKEVYLAY	447
QY	73	DEALGFTLVLSVFGAFVAVLTAVTVIHRHPLVNASDWQLGFLIQVSLIMLLSSMLF	132
Db	448	DEALGFTLVLSVFGAFVAVLTAVTVIHRHPLVNASDWQLGFLIQVSLIMLLSSMLF	507
QY	133	IDKPHNWSWAGQVTLALGFSCLSLCKGTSLSFLAYRISKSKTQLTSMHPLYRKIIVL	192
Db	508	IDKPHNWSWAGQVTLALGFSCLSLCKGTSLSFLAYRISKSKTQLTSMHPLYRKIIVL	567
QY	193	ISVLABIGICTAYLILEPMPVYKNMESQNTKIILGCNEISIEFLYMFIDAFLLLCFL	252
Db	568	ISVLABIGICTAYLILEPMPVYKNMESQNTKIILGCNEISIEFLYMFIDAFLLLCFL	627
QY	253	TTFVARQLPDNYEGKCTTFGLVFFIIMWSFVYVLTSTGKPKMAVEIFAILASSHGLL	312
Db	628	TTFVARQLPDNYEGKCTTFGLVFFIIMWSFVYVLTSTGKPKMAVEIFAILASSHGLL	687

QY 313 GCIFAPKCLIIILRRPNTSIVGRVSTTDCNCLQISAFVSSSELNNTVSTVLDRLVLI 372
 DB 688 GCIFAPKCLIIILRRPNTSIVGRVSTTDCNCLQISAFVSSSELNNTVSTVLDRLVLI 747
 QY 373 YMCPLKQLQ 380
 DB 748 YMCPLKQLQ 755

RESULT 2
 Q8TDUI PRELIMINARY; PRT; 365 AA.
 AC Q8TDUI;
 DT 01-JUN-2002 (TremBLrel. 21, Created)
 DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE Putative G-protein coupled receptor.
 GN Name=GPCR;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Takeda S., Kadowaki S., Haga T., Takasasu H., Mitaku S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB083610; BAB89323.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR Pfam; PF00003; 7tm 3; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 KW Receptor.
 SQ SEQUENCE 365 AA; 40920 MW; 9BFC4F8EFA873133 CRC64;

Query Match 88.1%; Score 1749; DB 2; Length 365;
 Best Local Similarity 99.1%; Pred. No. 2e-119;
 Matches 341; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 37 VSRPGERECQCGEDYWSNAQSECVLKEVEYLAYDEALGFTLVLSVFGAFVLA 96
 DB 22 VLRSTGERECQCGEDYWSNAQSECVLKEVEYLAYDEALGFTLVLSVFGAFVLA 81
 QY 97 VVTHRHPLVNASDWQLGFLIQVLSLIIMLSSMLFIDKPHNSCMAGQVTLALGFS 156
 DB 82 VVTHRHPLVNASDWQLGFLIQVLSLIIMLSSMLFIDKPHNSCMAGQVTLALGFS 141
 QY 157 SLLGKTSFLAYRISKSKTQTSMPHLYRKIVLISVLAIEGICTAYLILEPPMVYKN 216
 DB 142 SLLGKTSFLAYRISKSKTQTSMPHLYRKIVLISVLAIEGICTAYLILEPPMVYKN 201
 QY 217 MESQNTKIILGCNEISIEFLYMPGIDAFALICFTTFVARQLPDNYEGKCIITGMLV 276
 DB 202 MESQNTKIILGCNEISIEFLYMPGIDAFALICFTTFVARQLPDNYEGKCIITGMLV 261
 QY 277 FFIWMSFPVYLTGKGFMAVEIFAILASSHGLGCIIPAKCLIIILRRPNTSIVC 336
 DB 262 FFIWMSFPVYLTGKGFMAVEIFAILASSHGLGCIIPAKCLIIILRRPNTSIVC 321
 QY 337 GRVSTTDCNCLQISAFVSSSELNNTVSTVLDRLVLYMCPLKQLQ 380
 DB 322 GRVSTTDCNCLQISAFVSSSELNNTVSTVLDRLVLYMCPLKQLQ 365

RESULT 3
 Q70413 PRELIMINARY; PRT; 428 AA.
 AC Q70413;
 DT 01-AUG-1998 (TremBLrel. 07, Created)
 DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)

DE Putative pheromone receptor V2R2 (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vomeronasal neurons;
 RX MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
 RA Ryba N.J., Tirindelli R.;
 RT "A new multigene family of putative pheromone receptors.";
 RL Neuron 19:371-379(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vomeronasal neurons;
 RA Ryba N.J.P., Tirindelli R.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF053989; AAC08416.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR Pfam; PF00003; 7tm 3; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 KW Receptor.
 FT NON TER 1
 SQ SEQUENCE 428 AA; 47708 MW; EBF69A78F750E202 CRC64;

Query Match 73.0%; Score 1450; DB 2; Length 428;
 Best Local Similarity 75.5%; Pred. No. 1.4e-97;
 Matches 277; Conservative 35; Mismatches 55; Indels 0; Gaps 0;

QY 2 PHSVCTDVCPGTRGTFVQREPICCDFDIPCADGHVSRKPGERECECCGEDYWSNAQSE 61
 DB 62 PDSFCTQVCPPGTRKGIROGPICCFDCIFCADGVSENPQRECDPCGEDDWSNAEKS 121
 QY 62 CVLKEVEYLAYDEALGFTLVLSVFGAFVLA 121
 DB 122 CVPLKEVEYLAYDEALGFTLVLSVFGAFVLA 181
 QY 122 LIIMLSSMLFIDKPHNSCMAGQVTLALGFSICLCLGKTSFLAYRISKSKTQTS 181
 DB 182 LVITVLSMLFIDKSNWTCMARQVTLALGFCICLSTLGTISLPAYRISKSKTQTS 241
 QY 182 MHPYRKIVLISVLAIEGICTAYLILEPPMVYKNMESQNTKIILGCNEISIEFLYMPG 241
 DB 242 MSPYRKIVLISVLAIEGICTAYLILEPPMVYKNMESQNTKIILGCNEISIEFLYMPG 301
 QY 242 IDAFALICFTTFVARQLPDNYEGKCIITGMLVFIWMSFPVYLTGKGFMAVEI 301
 DB 302 FDVFLALICFTTFVARQLPDNYEGKCIITGMLVFIWMSFPVYLTGKGFMAVEI 361
 QY 302 FALASSHGLGCIIPAKCLIIILRRPNTSIVCGRVSTTDCNCLQISAFVSSSELNNT 361
 DB 362 FALASSHGLGCIIPAKCLIIILRRPNTSIVCGRVSTTDCNCLQISAFVSSSELNNT 421
 QY 362 VSTVLD 368
 DB 422 VSTVLD 428

RESULT 4
 Q70410 PRELIMINARY; PRT; 912 AA.
 AC Q70410;
 DT 01-AUG-1998 (TremBLrel. 07, Created)
 DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE Putative pheromone receptor V2R2.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP [1]
RC SEQUENCE FROM N.A.
RX TISSUE=Vomeroneasal neurons;
RY MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
RA Ryba N.J., Tirindelli R.;
RT "A new multigene family of putative pheromone receptors.";
RL Neuron 19:371-379(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeroneasal neurons;
RA Ryba N.J.P., Tirindelli R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053986; AAC08413.1;
DR HSSP; P23385; LEWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000068; Ca_sens receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 912 AA; 102348 MW; 2C54FAB6DFBFA48D CRC64;

Query Match 72.7%; Score 1444; DB 2; Length 912;
Best Local Similarity 74.7%; Pred. No. 8e-97;
Matches 274; Conservative 37; Mismatches 56; Indels 0; Gaps 0;

QY 2 PHSVCTDVCPPGTRGFGVQREPCPCDPSIPCADGHVSRKPGRECCQCGEDYWSNAQKSE 61
DB 546 PDSFCTQVCPGTRKGIQOQPICCFDCIPCADGVYSEKSGQRECDPCGEDDWSNAGKSK 605

QY 62 CVLKEVYLAYDEALGFTLVLSVFCAPVLAATVATVYVHRHTPLVNASDWLQGLFIQVS 121
DB 606 CVPKLVFEFLAYGALGFTLVLSIFGALVLAATVYVYVHRHTPLVNASDWLQGLFIQVS 665

QY 122 LIIMLSSMFLIDKPNWSCAGQVTLALGFSCLSLGKTSLLFLAYRISKSTQLTLS 181
DB 666 LVITVLSLFLIKPCNWCAGQVTLALGFSCLSLGKTSLLFLAYRISKSTQLTLS 725

QY 182 MHPLXKRIIVLSVLAIEIGICTAYLLEPPMVYKNMESQNTKIIIGCNBISIEFLYSMFG 241
DB 726 MHPIPKLIVLCVVGIEIGVCAAYLVLEPPRMFKNIEIQNVKIIPECNBSVEFLCSIFG 785

QY 242 IDAFLALLCFLTTFVARQLPDNYEGKCTIFGMLVFFIWMSPVPLSTGKPKFMAVEI 301
DB 786 FDLVRLALLCFLTTFVARQLPDNYEGKCTIFGMLVFFIWMSPVPLSTGKPKFMAVEI 845

QY 302 FALASSHGLGICFAPKCLIIILRPENTSETVCGRVSTTDCNICTLSAFVSSSELNNTT 361
DB 846 FALASSYGLGCLFLPKFCLIIILRPENTSETVCGRVSTTDCNICTLSAFVSSSELNNTT 905

QY 362 VSTVLDD 368
DB 906 VSTVLDE 912

RESULT 5
O70414 PRELIMINARY; PRT; 230 AA.
AC O70414;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE Putative pheromone receptor V2R2B (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP [1]
RC SEQUENCE FROM N.A.
RX TISSUE=Vomeroneasal neurons;
RY MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
RA Ryba N.J., Tirindelli R.;
RT "A new multigene family of putative pheromone receptors.";
RL Neuron 19:371-379(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeroneasal neurons;
RA Ryba N.J.P., Tirindelli R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053990; AAC08417.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
FT NON TER
SQ SEQUENCE 230 AA; 25703 MW; 2748EF5F4D72F404 CRC64;

Query Match 45.5%; Score 904.5; DB 2; Length 230;
Best Local Similarity 76.6%; Pred. No. 4.1e-58;
Matches 177; Conservative 20; Mismatches 33; Indels 1; Gaps 1;

QY 138 NWSMAGQVTLALGFSCLSLGKTSLLFLAYRISKSTQLTSMHPLXKRIIVLSVLA 197
DB 1 NWTMARQVTLALGFSCLSLGKTSLLFLAYRISKSTQLTSMHPLXKRIIVLSVLA 60

QY 198 EIGICTAYLLEPPMVYKNMESQNTKIIIGCNBISIEFLYSMFGIDAFLLCFLTTFVA 257
DB 61 EIGVCTAYLMLKPPRMVKNIEPQNVKIIPECNBSIEFLCSIFAPADVLLALLCFLTTFVA 120

QY 258 ROLPDNYEGKCTIFGMLVFFIWMSPVPLSTGKPKFMAVEI FALASSHGLGICF 317
DB 121 RKLDPNYEGKCTIFGMLVFFIWMSPVPLSTGKPKFMAVEI FALASSYGLGICF 180

QY 318 PKCLIIILRPENTSETVCGRVSTTDCNICTLSAFVSSSELNNTTSTVLDD 368
DB 181 PKCFIILLRPRNTDETGVGRVPTVDRSIQLASTSVSSEL-NTTSTVLDE 230

RESULT 6
O93555 PRELIMINARY; PRT; 458 AA.
AC O93555;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative odorant receptor (Fragment).
GN Name=GPB7;
OC Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Olfactory epithelium;
RY MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
RA Cao Y., Oh B.C., Stiver L.;
RT "Cloning and localization of two multigene receptor families in goldfish olfactory epithelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
DR EMBL; AF083084; AAC64079.1; -.


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DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR InterPro; IPR004073; Vmron_receptor2.
DR Pfam; PF000003; 7tm_3; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRGR.
DR PRINTS; PR01535; VOMERONASL2R.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
DR RECEPTOR.
DR NON_TER.
DR SEQUENCE 362 AA; 40359 MW; BFF09201800FC13P CRC64;
Query Match 39.0%; Score 775.5; DB 2; Length 362;
Best Local Similarity 42.9%; Pred. No. 1.6e-48;
Matches 146; Conservative 71; Mismatches 122; Indels 1; Gaps 1;
QY 1 LPHSVCTDVCPPGTGRGVQREPICCFDSIPCADGHVSRKPGRECEQCQGEDYWSNAQKS 60
DB 18 VPSVCSDSLCPGTRKAVKNGRPVCCYDCINCADGSEISNETDSDLCHECLPEYWPNNKKD 77
QY 61 ECVLKEVEYLAVDEALGFTLVLSVFGAFVLAATAVYVHRTPLVNASDWOLGFLIQV 120
DB 78 KCLPKPVEFLSWDDILGIIAFAVSAGSLVALSITLVFYKNTSPITVKANNSELSFLLLF 137
QY 121 SLIIMLSSMLFIDKPHNWSMAGQVTLALGFSCLSLGKTSSFLAYRISKSTOLT 180
DB 138 SLTSLFCLALTIFGRPTENSCMLRHTAFGTFVLCISCVLGKTIIVVLIAPKATLPGSNVM 197
QY 181 S-MHPLYRKIIVLISVLAIEGICTAYLILEPPMVYNNMESONTKIIILGNCNEISIEPLYSM 239
DB 198 KWFGLPQRLSVLQVLTAVLQVLCVLMKIYPPPPYNNMHQYKEKIIIECSLSAIGLWAV 257
QY 240 FGIDAFALICLTTFVARQLPDNYVEGKCTIFGMLVFPFIIWMSFVPLVSTKGKPKMAV 299
DB 258 LGVIGLAFLCFVLAFLARKLPDNFNEAKFITFSLMIFCAVWITFIPSVSPGKFTVAV 317
QY 300 EIPAILASSHGLGICFAPKCLIIILRPERNTSEIVCGRV 339
DB 318 EIPAILASSFGLILCIPAPKCFIIVFRPEQNTKKHLMGV 357
RESULT 9
O93558 PRELIMINARY; PRT; 408 AA.
AC O93558;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Putative odorant receptor (Fragment).
GN Names=GFBI4;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
RA Cao Y., Oh B.C., Stryer L.;
RT "Cloning and localization of two multigene receptor families in
goldfish olfactory epithelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
DR EMBL; AF083088; A083088.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007216; P:metabotropic glutamate receptor signaling p. . .; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR InterPro; IPR004073; Vmron_receptor2.
DR Pfam; PF000003; 7tm_3; 1.
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DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRGR.
DR PRINTS; PR01535; VOMERONASL2R.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
DR RECEPTOR.
DR NON_TER.
DR SEQUENCE 408 AA; 45418 MW; 8A61P477475PB24B CRC64;
Query Match 39.0%; Score 775.5; DB 2; Length 408;
Best Local Similarity 42.9%; Pred. No. 1.8e-48;
Matches 146; Conservative 71; Mismatches 122; Indels 1; Gaps 1;
QY 1 LPHSVCTDVCPPGTGRGVQREPICCFDSIPCADGHVSRKPGRECEQCQGEDYWSNAQKS 60
DB 64 VPSVCSDSLCPGTRKAVKNGRPVCCYDCINCADGSEISNETDSDLCHECLPEYWPNNKKD 123
QY 61 ECVLKEVEYLAVDEALGFTLVLSVFGAFVLAATAVYVHRTPLVNASDWOLGFLIQV 120
DB 124 KCLPKPVEFLSWDDILGIIAFAVSAGSLVALSITLVFYKNTSPITVKANNSELSFLLLF 183
QY 121 SLIIMLSSMLFIDKPHNWSMAGQVTLALGFSCLSLGKTSSFLAYRISKSTOLT 180
DB 184 SLTSLFCLALTIFGRPTENSCMLRHTAFGTFVLCISCVLGKTIIVVLIAPKATLPGSNVM 243
QY 181 S-MHPLYRKIIVLISVLAIEGICTAYLILEPPMVYNNMESONTKIIILGNCNEISIEPLYSM 239
DB 244 KWFGLPQRLSVLQVLTAVLQVLCVLMKIYPPPPYNNMHQYKEKIIIECSLSAIGLWAV 303
QY 240 FGIDAFALICLTTFVARQLPDNYVEGKCTIFGMLVFPFIIWMSFVPLVSTKGKPKMAV 299
DB 304 LGVIGLAFLCFVLAFLARKLPDNFNEAKFITFSLMIFCAVWITFIPSVSPGKFTVAV 363
QY 300 EIPAILASSHGLGICFAPKCLIIILRPERNTSEIVCGRV 339
DB 364 EIPAILASSFGLILCIPAPKCFIIVFRPEQNTKKHLMGV 403
RESULT 10
O93552 PRELIMINARY; PRT; 844 AA.
AC O93552;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative odorant receptor.
GN Name=GFBI;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
RA Cao Y., Oh B.C., Stryer L.;
RT "Cloning and localization of two multigene receptor families in
goldfish olfactory epithelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
DR EMBL; AF083088; A083088.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007216; P:metabotropic glutamate receptor signaling p. . .; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000345; GPCR_Mgr.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR InterPro; IPR004073; Vmron_receptor2.
DR Pfam; PF000003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
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SQ SEQUENCE 880 AA; 97463 MW; 8F5C02444175500A CRC64;
Query Match 37.9%; Score 753.5; DB 2; Length 880;
Best Local Similarity 41.9%; Pred. No. 1.5e-46;
Matches 139; Conservative 69; Mismatches 123; Indels 1; Gaps 1;
QY 1 LPHSVCTDVCPTGTGTFVORBEIPCCPDSIPCADGHVSRKPGRECEQCEQEDYWSNAQKS 60
DB 538 VPLSVCSICPPGTGTRKAIENYPIICCHDCVCTAGISNOTDAIECARCLPEFWSNADRT 597
QY 61 ECVLKEVEYLAVDEALGFTLVILSVFGAFVVLAVTAVVYVHRTPLVNASDMDGLFLIOV 120
DB 598 ACVPKQVEFLSGFTGIALVSLGSLFUTCAVLFVFFHRTSPVIRANNSLSLELLF 657
QY 121 SLIIMLSSMLFIDKPHNWSMAGQVTLALGFSCLSLGKTSFLAYRISKSTQLT 180
DB 658 SLTLCFLCSLTFTISPPSQMSCLRHATFAGITFVLICISLIGKTIIVLMAPRATLPQSDVM 717
QY 181 S-MHPLYRKIIIVLSVLAEGICTAVILIEPPMVYKMSQNTKIILGCNEISIEFLYM 239
DB 718 KWFPGPKQKAIITFTLVQVVICVTLVAVAPTPRQVMPRESAIIILLCDGSTIAFSLV 777
QY 240 FGIADAFALACELTTFVARQLPDNYEGKCIITFGMLVFFIIMWSFVPLVSTKGEKMAV 299
DB 778 LGVIGVACMCFLLAFARLKLDPNFENARLAFMIFCAVWVAFVAFVAYISPGKYSTLT 837
QY 300 EIFAILASSHGLGCIAPKPKLIILARPERNT 331
DB 838 EIFAILASSYGLGCIAPKPKCYIILMKSEKNT 869

RESULT 13

073640 PRELIMINARY; PRT; 875 AA.
AC 073640;
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Phomone receptor.
GN Names=Cal5.1;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98226788; PubMed=9560249; DOI=10.1073/pnas.95.9.5178;
RA Naito T., Saito Y., Yamamoto J., Nozaki Y., Tomura K., Hazama M.,
RA Nakanishi S., Brenner S.;
RT "Putative phomone receptors related to the Ca2+-sensing receptor in
RT Fugu."
RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
DR EMBL; AB008862; BAA26127.1; -;
DR HSPB; P23385; 1EWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007216; P:metabotropic glutamate receptor signaling p. . .; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR InterPro; IPR004073; Vmron_receptor2.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR01535; VOMERONASL2R.
DR PROSITE; PS00981; G PROTEIN RECP F3_3; 1.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 875 AA; 94933 MW; 7A4DD782B170A405 CRC64;

Query Match 37.6%; Score 747; DB 2; Length 856;

Query Match 37.8%; Score 751; DB 2; Length 875;
Best Local Similarity 42.1%; Pred. No. 2.3e-46;
Matches 142; Conservative 73; Mismatches 118; Indels 4; Gaps 2;
QY 1 LPHSVCTDVCPTGTGTFVORBEIPCCPDSIPCADGHVSRKPGRECEQCEQEDYWSNAQKS 60
DB 534 VPLSVCSICPPGTGTRKAIENYPIICCHDCVCTAGISNOTDAIECARCLPEFWSNADRT 593
QY 61 ECVLKEVEYLAVDEALGFTLVILSVFGAFVVLAVTAVVYVHRTPLVNASDMDGLFLIOV 120
DB 594 ACVPKQVEFLSGFTGIALVSLGSLFUTCAVLFVFFHRTSPVIRANNSLSLELLF 653
QY 121 SLIIMLSSMLFIDKPHNWSMAGQVTLALGFSCLSLGKTSFLAYRISK--SKTQ 178
DB 654 SLKLCFLCSLVLFGPSVWSCRFOQAAGISFVLCVSLQVKTIVVLAAPRSARPGAGAL 713
QY 179 LTSMHPLYRK--IIVLSVLAEGICTAVILIEPPMVYKMSQNTKIILGCNEISIEFL 236
DB 714 KWFPGPSQKQKAIITFTLVQVVICVTLVAVAPTPRQVMPRESAIIILLCDGSTIAFSLV 773
QY 237 YSMFGIDAFALACELTTFVARQLPDNYEGKCIITFGMLVFFIIMWSFVPLVSTKGEK 296
DB 774 SLVGVIGLACTCLLAFARLKLDPNFENAKLITFSLIFCAVWVAFVAFVAYISPGKYS 833
QY 297 MAVEIPAILASSHGLGCIAPKPKLIILARPERNTSE 333
DB 834 VAVEIPAILASSYGLGCIAPKPKFILLRPERKTKK 870

RESULT 14

073638 PRELIMINARY; PRT; 856 AA.
AC 073638;
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Phomone receptor.
GN Names=Cal2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98226788; PubMed=9560249; DOI=10.1073/pnas.95.9.5178;
RA Naito T., Saito Y., Yamamoto J., Nozaki Y., Tomura K., Hazama M.,
RA Nakanishi S., Brenner S.;
RT "Putative phomone receptors related to the Ca2+-sensing receptor in
RT Fugu."
RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
DR EMBL; AB008860; BAA26125.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007216; P:metabotropic glutamate receptor signaling p. . .; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR01535; VOMERONASL2R.
DR PROSITE; PS00981; G PROTEIN RECP F3_3; 1.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 856 AA; 94590 MW; 7794C3E3DA143E18 CRC64;

Query Match 37.6%; Score 747; DB 2; Length 856;

Best Local Similarity 42.6%; Pred. No. 4.4e-46;		Matches 144; Conservative 64; Mismatches 128; Indels 2; Gaps 2;	
QY	2	PHSVCTDVPCTGRGFWQREPIPCFDSIPCADGHVSRKPGERECEQCGEDYWSNAQSE	61
DB	516	PLSVCSQSCIFGPRQAVIKGPKFCPTCVACAAGEISNSNSAECIQCPLPEFWSNEDHSQ	575
QY	62	CVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVVYHRRHTPLVNASDWOLGFLIQVS	121
DB	576	CVPKVIEPLSEETWGAALLAVSLFGAALTSVFCVFRFRHTPLVNASSELSFLLIFS	635
QY	122	LIIMLLSMLFIDKPHNWSMAGVTLALGFSCLSLGKTSFLAYRISK-SKTQLT	180
DB	636	LTCLFCLSLTFIGRPSRWSCVLRHTAFGITFALCMSCVLAKTVAVLFAFTAKRPGNTVYF	695
QY	181	SMHPLYRKIIIVLSVLAIEIGICTAYLILEPMPVYKNMESONTKIILGCNEISTEFLYSMF	240
DB	696	CSVPLQR-TSVFACITILQVILCVLMLTAPHPHKNHTAHAKERIILILECNLGSVPWFVVL	754
QY	241	GIDAFALLCLFLLTFVARQLPDNYEGKCTIFGMLVFFIIMWSFVVPVYLSTKKGKMAVE	300
DB	755	GYIGLLAVICILAFILARKLPDNEAKFITFSMLIFCAVAVTFIPAYVSSPKFTVAVE	814
QY	301	IFAILASSHGLGCTFAPKCLIIILLRPERNTSEIVCGR	338
DB	815	IFAILASSFGLFCIFAPKCVILILKPEKNTKHHMGR	852

RESULT 15

ID	Q8J104	PRELIMINARY; PRT; 1027 AA.
AC	Q8J104;	
DT	01-OCT-2002 (TrenBMLrel. 22, Created)	
DT	01-OCT-2002 (TrenBMLrel. 26, Last sequence update)	
DE	Calcium polyvalent cation receptor/salinity sensing protein.	
OS	Squalus acanthias (Spiny dogfish).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;	
OC	Elasmobranchii; Squalae; Hypnosqualea; Squaliformes; Squaloidei;	
OC	Squalidae; Squalus.	
OX	NCHI_TaxID=7797;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Kidney;	
RX	MEDLINE=22103704; PubMed=12093923; DOI=10.1073/pnas.152294399;	
RA	Nearing J., Betka M., Quinn S., Hentschel H., Elger M., Baum M.,	
RA	Bai M., Chattopadhyay N., Brown E.M., Hebert S.C., Harris H.W.;	
RT	"Polyvalent cation receptor proteins (CaRs) are salinity sensors in	
RT	fish."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:9231-9236(2002).	
DR	EMBL; AF406649; AAM7700.1; -.	
DR	HSSP; P23385; 1ISS.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0008067; F:metabotropic Glutamate, GABA-B-like recepto. . . ; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	InterPro; IPR001828; ANF_receptor.	
DR	InterPro; IPR000068; Ca_sens_receptor.	
DR	InterPro; IPR000337; GPCR_Mgr.	
DR	InterPro; IPR011500; NCD3G_GPCR.	
DR	Pfam; PF00003; 7tm_3; 1.	
DR	Pfam; PF01094; ANF_receptor; 1.	
DR	Pfam; PF07562; NCD3G; 1.	
DR	PRINTS; PR00592; CASENSINGR.	
DR	PRINTS; PR00248; GPCRMR.	
DR	PROSITE; PS00979; G_PROTEIN_RECPE_F3_1; 1.	
DR	PROSITE; PS00980; G_PROTEIN_RECPE_F3_2; UNKNOWN_1.	
DR	PROSITE; PS00981; G_PROTEIN_RECPE_F3_3; 1.	
DR	PROSITE; PS00981; G_PROTEIN_RECPE_F3_4; 1.	
DR	PROSITE; PS00981; G_PROTEIN_RECPE_F3_5; 1.	
KW	Receptor.	
QY	SEQUENCE 1027 AA; 114412 MW; 189FF1E323B5B7C7 CRC64;	

Query Match 37.1%; Score 736.5; DB 2; Length 1027;
Best Local Similarity 38.7%; Pred. No. 3e-45;

Matches 148; Conservative 73; Mismatches 134; Indels 27; Gaps 5;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																</
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